



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

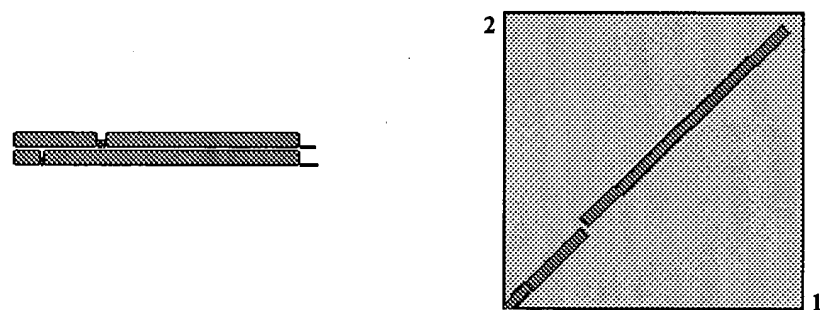
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.000** wordsize: **3** Filter: ☒ View option: **Standard**
 Masking character option: **X for protein, n for nucleotide** Masking color option: **Black**
☐ Show CDS translation **Align**

Sequence 1: **lc|seq_1**
 Length = 183 (1 .. 183)

Sequence 2: **gi|1717863|sp|P52491|UBC12_YEAST|NEDD8-conjugating enzyme UBC12 (RUB1-conjugating enzyme) (RUB1-protein ligase) (Ubiquitin carrier protein 12).**
 Length = 188 (1 .. 188)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 153 bits (386), Expect = 5e-36
 Identities = 76/179 (42%), Positives = 114/179 (63%), Gaps = 8/179 (4%)

```
Query 1  MIKLFSLKQQKKEESAGGTKGSSKKASAAQLRIQKDINELNLPKTCDISF-----SDP  54
          M+KL L+++K++E   +   SAA++R+++D++ L+LP T ++   +D
Sbjct 1  MLKLRQLQKKKQKENE--NSSSIQPNLSAARIRLKRDLSDLPPTVTNLNVITSPDSADR  58

Query 55  DLLNFKLVICPDGEFGYKSGKFVFSFKVGQGYPHDPPKVKCETMVYHPNIDLEGNVCLNI  114
          ++++ PDEG+Y  G  F+   + YP +PPKV C  ++HPNIDL+GNVCLNI
Sbjct 59  SQSPKLEVIVRPDEGYNYGSINFNLDNEVYPIEPPKVCLKKIFHPNIDLKGNVCLNI  118

Query 115 LREDWKPVLTINSIIYGLQYLFLEPNPDPLNKEAAEVLQNNRRLFEQNVQSRMGGYI  173
          LREDW P L + SII GL +LFLEPNP DPLNK+AA++L   + F + V+ +M GG I
Sbjct 119 LREDWSPALDLSIITGLLFLFLEPNPDPLNKDAAKLLCEGEKEFAEAVRLTMSGGSI  177
```

CPU time: 0.02 user secs. 0.00 sys. secs 0.02 total secs.

Lambda K H
 0.318 0.138 0.411

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 302

Blast Result

Number of extensions: 163
Number of successful extensions: 2
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 183
Length of database: 1,238,154,749
Length adjustment: 125
Effective length of query: 58
Effective length of database: 1,238,154,624
Effective search space: 71812968192
Effective search space used: 71812968192
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 74 (33.1 bits)

RESULT 1

UBE2M_HUMAN

ID UBE2M_HUMAN STANDARD; PRT; 183 AA.
AC P61081; O76069; Q8VC50;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ubiquitin-conjugating enzyme E2 M (EC 6.3.2.19) (Ubiquitin-protein
DE ligase M) (Ubiquitin carrier protein M) (Nedd8-conjugating enzyme
DE Ubc12).
GN Name=UBE2M; Synonyms=UBC12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RA Gong L., Yeh E.T.H.;
RT "Identification of the activating and conjugating enzymes of the
RT NEDD8-conjugation pathway.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98361870; PubMed=9694792;
RA Osaka F., Kawasaki H., Aida N., Saeki M., Chiba T., Kawashima S.,
RA Tanaka K., Kato S.;
RT "A new NEDD8-ligating system for cullin-4A.";
RL Genes Dev. 12:2263-2268(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Catalyzes the covalent attachment of ubiquitin-like
 CC protein NEDD8 to other proteins.
 CC -!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
 CC diphosphate + protein N-ubiquityllysine.
 CC -!- PATHWAY: Ubiquitin conjugation; second step.
 CC -!- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AF075599; AAC26141.1; -; mRNA.
 DR EMBL; AB012191; BAA33145.1; -; mRNA.
 DR EMBL; BT006754; AAP35400.1; -; mRNA.
 DR EMBL; BC058924; AAH58924.1; -; mRNA.
 DR PDB; 1TT5; X-ray; E/F=1-26.
 DR PDB; 1Y8X; X-ray; A=27-183.
 DR SMR; P61081; 27-183.
 DR Ensembl; ENSG00000130725; Homo sapiens.
 DR HGNC; HGNC:12491; UBE2M.
 DR MIM; 603173; -.
 DR InterPro; IPR000608; UBQ-conjugat_E2.
 DR Pfam; PF00179; UQ_con; 1.
 DR ProDom; PD000461; UBQ_conjugat; 1.
 DR SMART; SM00212; UBCC; 1.
 DR PROSITE; PS00183; UBIQUITIN_CONJUGAT_1; 1.
 DR PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
 KW 3D-structure; Ligase; Multigene family; Ubl conjugation pathway.
 FT ACT_SITE 111 111 Glycyl thioester intermediate (By
 FT similarity).
 SQ SEQUENCE 183 AA; 20900 MW; E3C288CA6A98BC5C CRC64;

Alignment Scores:

Pred. No.:	9.77e-81	Length:	183
Score:	970.00	Matches:	183
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	96.3%	Indels:	0
DB:	1	Gaps:	0

US-10-681-690-3 (1-552) x UBE2M_HUMAN (1-183)

Qy	1	ATGATCAAGCTGTTCTCGCTGAAGCAGCAGAAGAAGGAGGAGGAGTCGGCGGGCGGCACC	60
Db	1	MetIleLysLeuPheSerLeuLysGlnGlnLysLysGluGluGluSerAlaGlyGlyThr	20
Qy	61	AAGGGCAGCAGCAAGAAGGCGTCGGCGGCGCAGCTGCGGATCCAGAAGGACATAAACGAG	120
Db	21	LysGlySerSerLysLysAlaSerAlaAlaGlnLeuArgIleGlnLysAspIleAsnGlu	40

Qy	121	CTGAACCTGCCCAAGACGTGTGATATCAGCTTCTCAGATCCAGACGACCTCCTCAACTTC	180
Db	41	LeuAsnLeuProLysThrCysAspIleSerPheSerAspProAspAspLeuLeuAsnPhe	60
Qy	181	AAGCTGGTCATCTGTCTGATGAGGGCTTCTACAAGAGTGGGAAGTTTGTGTTTCAGTTTT	240
Db	61	LysLeuValIleCysProAspGluGlyPheTyrLysSerGlyLysPheValPheSerPhe	80
Qy	241	AAGGTGGGCCAGGGTTACCCGCATGATCCCCCAAGGTGAAGTGTGAGACAATGGTCTAT	300
Db	81	LysValGlyGlnGlyTyrProHisAspProProLysValLysCysGluThrMetValTyr	100
Qy	301	CACCCCAACATTGACCTCGAGGGCAACGTCTGCCTCAACATCCTCAGAGAGGACTGGAAG	360
Db	101	HisProAsnIleAspLeuGluGlyAsnValCysLeuAsnIleLeuArgGluAspTrpLys	120
Qy	361	CCAGTCCTTACGATAAACTCCATAATTTATGGCCTGCAGTATCTCTTCTGGAGCCCAAC	420
Db	121	ProValLeuThrIleAsnSerIleIleTyrGlyLeuGlnTyrLeuPheLeuGluProAsn	140
Qy	421	CCCGAGGACCCACTGAACAAGGAGGCCGCAGAGGTCCTGCAGAACAACCGGCGGCTGTTT	480
Db	141	ProGluAspProLeuAsnLysGluAlaAlaGluValLeuGlnAsnAsnArgArgLeuPhe	160
Qy	481	GAGCAGAACGTGCAGCGCTCCATGCGGGGTGGCTACATCGGCTCCACCTACTTTGAGCGC	540
Db	161	GluGlnAsnValGlnArgSerMetArgGlyGlyTyrIleGlySerThrTyrPheGluArg	180
Qy	541	TGCCTGAAA	549
Db	181	CysLeuLys	183